PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,826

DATE: 05/21/2002
TIME: 15:40:34

Input Set : A:\620-179.app
Output Set: N:\CRF3\05212002\J018826.raw

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  3 <110> APPLICANT: Davis, Peter D
  5 <120> TITLE OF INVENTION: Chimeric proteins mediating targeted apoptosis
  7 <130> FILE REFERENCE: 620-179
  9 <140> CURRENT APPLICATION NUMBER: US 10/018,826
C--> 10 <141> CURRENT FILING DATE: 2002-04-22
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02449
 13 <151> PRIOR FILING DATE: 2000-06-26
 15 <150> PRIOR APPLICATION NUMBER: GB 9914650.8
 16 <151> PRIOR FILING DATE: 1999-06-24
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
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 23 <211> LENGTH: 84
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
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 32              20                  25                  30
 34 Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu
 35          35                  40                  45
 37 Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu
 38      50                  55                  60
 40 Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
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 48 <211> LENGTH: 86
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
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 57              20                  25                  30
 59 Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met
 60          35                  40                  45
 62 Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu
 63      50                  55                  60
 65 Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
 66  65                  70                  75                  80
 68 Asp Ile Glu Glu Ala Leu
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78 <221> NAME/KEY: CDS
79 <222> LOCATION: (116)..(1411)
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
83       construct encoding a chimeric protein containing
84       the extracellular domain of CD44H and the
85       transmembrane and cytoplasmic domains of human Fas
87 <400> SEQUENCE: 3
88 ccagcctctg ccaggttcgg tccgccatcc tcgtcccgtc ctccgccggc ccctgccccg 60
90 cgcccaggga tcctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg  118
91                                                              Met
92                                                                1
94 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg   166
95 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
96               5                  10                  15
98 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta   214
99 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
100          20                  25                  30
102 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc   262
103 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
104      35                  40                  45
106 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag   310
107 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
108  50                  55                  60                  65
110 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc   358
111 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
112                  70                  75                  80
114 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt   406
115 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
116              85                  90                  95
118 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag   454
119 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
120          100                 105                 110
122 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt   502
123 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
124      115                 120                 125
126 aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata   550
127 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
128 130                 135                 140                 145
130 act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac   598
131 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr
132                 150                 155                 160
134 aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac   646
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136             165                 170                 175
138 gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac   694
139 Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr
140         180                 185                 190
142 atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt   742
143 Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser
144     195                 200                 205
146 ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa   790
147 Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln
148 210                 215                 220                 225
150 gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gga tct gaa   838
151 Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu
152                 230                 235                 240
154 tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc   886
155 Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr
156             245                 250                 255
158 tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ctt   934
159 Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu
160         260                 265                 270
162 tgt ctt ctt ctt ttg cca att cca cta att gtt tgg gtg aag aga aag   982
163 Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys
164     275                 280                 285
166 gaa gta cag aaa aca tgc aga aag cac aga aag gaa aac caa ggt tct  1030
167 Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser
168 290                 295                 300                 305
170 cat gaa tct cca acc tta aat cct gaa aca gtg gca ata aat tta tct  1078
171 His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser
172                 310                 315                 320
174 gat gtt gac ttg agt aaa tat atc acc act att gct gga gtc atg aca  1126
175 Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr
176             325                 330                 335
178 cta agt caa gtt aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc  1174
179 Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala
180         340                 345                 350
182 aaa ata gat gag atc aag aat gac aat gtc caa gac aca gca gaa cag  1222
183 Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln
184     355                 360                 365
186 aaa gtt caa ctg ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa  1270
187 Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu
188 370                 375                 380                 385
190 gcg tat gac aca ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act  1318
191 Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr
192                 390                 395                 400
194 ctt gca ggg aaa att cag act atc atc ctc aag gac att act agt gac  1366
195 Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp
196             405                 410                 415
198 tca gaa aat tca aac ttc aga aat gaa atc caa agc ttg gtc tag      1411
199 Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
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207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric protein
212       containing the extracellular domain of CD44H and the
213       transmembrane and cytoplasmic domains of human Fas
215 <400> SEQUENCE: 4
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219              20                  25                  30
220 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
221          35                  40                  45
222 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
223      50                  55                  60
224 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
225  65                  70                  75                  80
226 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
227                  85                  90                  95
228 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
229             100                 105                 110
230 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
231         115                 120                 125
232 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
233     130                 135                 140
234 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
235 145                 150                 155                 160
236 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
237                 165                 170                 175
238 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
239             180                 185                 190
240 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
241         195                 200                 205
242 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
243     210                 215                 220
244 Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser
245 225                 230                 235                 240
246 Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
247                 245                 250                 255
248 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
249             260                 265                 270
250 Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
251         275                 280                 285
252 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
253     290                 295                 300
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256 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
257                 325                 330                 335
258 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
259             340                 345                 350
260 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
261         355                 360                 365
262 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
263     370                 375                 380
264 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
265 385                 390                 395                 400
266 Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
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275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (116)..(1426)
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283 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
284       construct encoding a chimeric protein containing
285       the extracellular and transmembrane domains of CD44H
286       and the cytoplasmic domain of human Fas
288 <400> SEQUENCE: 5
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291 cgcccaggga tcctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg  118
292                                                              Met
293                                                               1
295 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg   166
296 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
297               5                  10                  15
299 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta   214
300 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
301           20                  25                  30
303 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc   262
304 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
305       35                  40                  45
307 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag   310
308 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
309   50                  55                  60                  65
311 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc   358
312 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
313                 70                  75                  80
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